Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-6. (Canceled)

Claim 7. (Currently amended) A method for identifying an agent that interacts with ER-β, the method comprising ~~the steps of~~:

(a) providing a crystal structure of ER- β having a resolution of 1.83 Å or less;

~~(a)~~ (b) generating a three dimensional model of ER-β using the relative structural coordinates according to Figure 2, ± a root mean square deviation from the backbone atoms of ~~said~~ the amino acids of not more than 1.5Å, the relative structural coordinates being based on the crystal structure of ER-β; and

~~(b)~~ (c) employing ~~said~~ the three-dimensional model to design or select an agent that interacts with ER-β.

Claim 8. (Currently amended) The method of claim 7, further comprising ~~the steps of~~:

~~(c)~~ (d) obtaining the ~~identified~~ agent; and

~~(d)~~ (e) contacting the ~~identified~~ agent with ER-β in order to determine the effect the agent has on ER-β activity.

Claim 9. (Currently amended) A method for identifying an activator or inhibitor of ~~a molecule or molecular complex comprising a genistein binding site~~ ER-β, the method comprising ~~the steps of~~:

(a) providing a crystal structure of ER-β having a resolution of 1.83 Å or less;

~~(a)~~ (b) generating a three dimensional model of ~~said molecule or molecular complex comprising a genistein binding site~~ ER-β using (i) the relative structural coordinates of amino acid residues MET343, LEU346, LEU349, GLU353, MET384, LEU387, MET388, ARG394, PHE404, ILE421, ILE424, GLY520, HIS523 and LEU524 according to Figure 2 for monomer A of ER-β, ± a root mean square deviation from the backbone atoms of ~~said~~ the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer A of ER-β being based on the crystal structure of ER-β or (ii) the relative structural coordinates of amino acid residues MET343, LEU346, LEU349, GLU353, MET384, LEU387, MET388, LEU391, ARG394, PHE404, ILE421, ILE424, GLY520, HIS523 and LEU524 according to Figure 2 for monomer B of ER-β, ± a root mean square deviation from the backbone atoms of ~~said~~ the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer B of ER-β being based on the crystal structure of ER-β; and

~~(b)~~ (c) selecting or designing a candidate activator or inhibitor by performing computer fitting analysis of the candidate activator or inhibitor with the three dimensional model generated in step ~~(a)~~ (b).

Claim 10. (Currently amended) The method of claim 9, wherein the structural coordinates according to (i) further ~~comprises~~ comprise the relative structural coordinates of amino acid residues VAL328, MET342, SER345, THR347, LYS348, LEU349, ALA350, ASP351, LEU354, MET357, TRP383, GLU385, VAL386, MET389, GLY390, LEU391, MET392, LEU402, ILE403, ALA405, LEU408, VAL418, GLU419, GLY420, LEU422, GLU423, PHE425, LEU428, ALA516, SER517, LYS519, MET521, GLU522, LEU525, ASN526, MET527, LYS528, VAL533, VAL535, TYR536 and LEU538 according to Figure 2 for monomer A of ER-β, ± a root mean square deviation from the backbone atoms of ~~said~~ the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer A of ER-β being based on the crystal structure of ER-β.

Claim 11. (Currently amended) The method of claim 9, wherein the relative structural coordinates according to (ii) further ~~comprises~~ comprise the relative structural coordinates of amino acid residues MET342, SER345, THR347, LYS348, ALA350, ASP351,

MET357, TRP383, GLU385, VAL386, LEU387, MET389, GLY390, MET392, LEU402, ILE403, ALA405, LEU408, VAL418, GLU419, GLY420, LEU422, GLU423, PHE425, LEU428, ALA516, SER517, LYS519, MET521, GLU522, LEU525, ASN526, MET527, LYS528, VAL533, TYR536 and LEU538 according to Figure 2 for monomer B of ER-β , ± a root mean square deviation from the backbone atoms of ~~said~~ the amino acids of not more than 1.5Å, the relative structural coordinates of the amino acid residues for monomer B of ER-β being based on the crystal structure of ER-β.

Claim 12. (Currently amended) The method of claim 9, ~~which~~ further ~~comprises~~ comprising the steps of:

~~(c)~~ (d) obtaining the candidate activator or inhibitor; and

~~(d)~~ (e) contacting the candidate activator or inhibitor with the molecule or molecular complex and determining the effect the candidate activator or inhibitor has on the molecule or molecular complex.

Claim 13. (Currently amended) The method of claim 12, wherein the candidate activator or inhibitor is contacted with the molecule or ~~molecule~~ molecular complex in the presence of genistein ~~in order~~ to determine the effect the candidate activator or inhibitor has on binding of the molecule or molecular complex to genistein.

Claims 14-15. (Canceled)

Claim 16. (New) The method of claim 7, wherein the crystal structure of ER-β has a resolution of 1.8 Å.

Claim 17. (New) The method of claim 9, wherein the crystal structure of ER-β has a resolution of 1.8 Å.